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1 M-----ARAKLPRSPSE-----GKAGPGGA-----PAGAAPEEHslo2
1 M-----ARAKLPRSPSE-----GKAGPGDT-----PAGSAAPEERSLACK
1 AREEGGSHSLPRVGSLLPGRMPLPDGARTPGGVCREARGGGYTNRTEFFDDGQCAPRRKIAA1422

30 P-HGLSPLLPARG--GGSVGSDV--GQRLPVEDFSLDSSLSQ--VQVEFYVNENTFKhslo2
30 P-HGLSPLLPTRG--GGSVGSDV--GQRLHVEDFSLDSSLSQ--VQVEFYVNENTFKrSLACK
61 PCAGDGALLDTAGFKMSDLDSEVLPLPPRYRFRDLLLGDPSFQNDDEVQVEFYVNENTFKKIAA1422

80 ERLKLFIFIKNQSSSLRIRLFNFSLKLLTCLLYIVRVLLDDPALGIGCWGCPKQNYSFNDShslo2
80 ERLKLFIFIKNQSSSLRIRLFNFSLKLLTCLLYIVRVLLDNDPDQIGIGCWGCTKYNYSFNDSrSLACK
121 ERLKLFIFIKNQSSSLRIRLFNFSLKLLTCLLYIVRVLLDDPALGIGCWGCPKQNYSFNDSKIAA1422

140 SSEINWAPILWVERKMTLWAIQVIVAIISPLETMLLIYLSYKGNIWEQIFRVSFVLEMINSlo2
140 SSEFHWAPILWVERKMTLWAIQVIVAIISFLETMLLIYLSYKGNIWEQIFHVSFVLEMINSrSLACK
181 SSEINWAPILWVERKMTLWAIQVIVAIISFLETMLLIYLSYKGNIWEQIFRVSFVLEMINSKIAA1422

200 TLPFIIITIFWPPPLRNLFIPVFLNCWLAKHALENMINDEFHRAILRTQSAMFNQVLIILECTLhslo2
200 TLPFIIITIFWPPPLRNLFIPVFLNCWLAKHALENMINDEFHRAILRTQSAMFNQVLIILECTLrSLACK
241 TLPFIIITIFWPPPLRNLFIPVFLNCWLAKHALENMINDEFHRAILRTQSAMFNQVLIILECTLKIAA1422

260 LCLVFTGTCGIQHLELAGENLSLTSFYFCIVTFTSTVGYGDVTPKIWPSSQLLVVIMICVAhslo2
260 LCLVFTGTCGIQHLELAGENLSLTSFYFCIVTFTSTVGYGDVTPKIWPSSQLLVVILICVTrSLACK
301 LCLVFTGTCGIQHLELAGENLSLTSFYFCIVTFTSTVGYGDVTPKIWPSSQLLVVIMICVAKIAA1422

320 LVVLPLQFEEELVYLWMERQKSGGNYSRHRAQTEKHVVLCVSSSLKIDLLMDFLNEFYAHPRhslo2
320 LVVLPLQFEEELVYLWMERQKSGGNYSRHRAQTEKHVVLCVSSSLKIDLLMDFLNEFYAHPRrSLACK
361 LVVLPLQFEEELVYLWMERQKSGGNYSRHRAQTEKHVVLCVSSSLKIDLLMDFLNEFYAHPRKIAA1422

380 LQDYYVVVILCPTEMDVQVRRVLQIPLWSQRVIYLYQGSALKDQDLMRAKMDNGEACFILSShslo2
380 LQDYYVVVILCPTSEMDVQVRRVLQIPLWSQRVIYLYQGSALKDQDLMRAKMDNGEACFILSSrSLACK
421 LQDYYVVVILCPTEMDVQVRRVLQIPLWSQRVIYLYQGSALKDQDLMRAKMDNGEACFILSSKIAA1422

440 RNEVDRTAADHQTIILRAWAVKDFAPNCPLYVQIILKPENKFHVKFADHVVCEECKYAMLAslo2
440 RNEVDRTAADHQTIILRAWAVKDFAPNCPLYVQIILKPENKFHVKFADHVVCEECKYAMLArSLACK
481 RNEVDRTAADHQTIILRAWAVKDFAPNCPLYVQIILKPENKFHVKFADHVVCEECKYAMLAKIAA1422

FIG. 1



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500 LNCICPATSTLITLLVHTSRGQEGQESPEQWQRMYGRCSGNEVYHIRMGD SKFFREYEGK hSlo2
500 LNCICPATSTLITLLVHTSRGQEGQESPEQWQRMYGRCSGNEVYHIRMGD SKFFREYEGK rSLACK
541 LNCICPATSTLITLLVHTSRGQEGQESPEQWQRMYGRCSGNEVYHIRMGD SKFFREYEGK KIAA1422

560 SFTYAAFAHKKYGVCLIGLKREDNKSILLNPGPRHILAAASDTCFYINITKEENSAFI FK hSlo2
560 SFTYAAFAHKKYGVCLIGLKREDNKSILLNPGPRHILAAASDTCFYINITKEENSAFI FK rSLACK
601 SFTYAAFAHKKYGVCLIGLKREDNKSILLNPGPRHILAAASDTCFYINITKEENSAFI FK KIAA1422

620 QEEKRKKRAFSGQGLHEGPARLPVHSIIASM--VAMD LQGTEHRPTQSGGGGGGSKLALP hSlo2
620 QEEKQNRGLAGQALYEGPSRLPVHSIIASM--VAMD LQNTDCRPSQGGSGGGGKLTLP rSLACK
661 QEEKRKKRAFSGQGLHEGPARLPVHSIIASMGTVAMD LQGT EHRPTQSGGGGGGSKLALP KIAA1422

678 TENGSGSRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP hSlo2
678 TENGSGSRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP rSLACK
722 TENGSGSRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP KIAA1422

738 YIVSSPTLCHLLPVKAPFCCLRLDKGCKHNSYEDAKAYGFKNKLIIVSAETAGNGLYNFI hSlo2
738 YIGSSPTLCHLLPVKAPFCCLRLDKGCKHNSYEDAKAYGFKNKLIIVSAETAGNGLYNFI rSLACK
781 YIGSSPTLCHLLPVKAPFCCLRLDKGCKHNSYEDAKAYGFKNKLIIVSAETAGNGLYNFI KIAA1422

798 VPLRAYYRSRKELNPIVLLLDNKPDDHFFLEAICCFPMVYYMEGSVDNLD SLLQCGIIYAD hSlo2
798 VPLRAYYRSRKELNPIVLLLDNKPDDHFFLEAICCFPMVYYMEGSVDNLD SLLQCGIIYAD rSLACK
841 VPLRAYYRSRKELNPIVLLLDNKPDDHFFLEAICCFPMVYYMEGSVDNLD SLLQCGIIYAD KIAA1422

858 NLVVVDKESTMSAEEDYMADAKTIVNVQTMFRLFPSLSITTELTHPSNMRFMQFRAKDSY hSlo2
858 NLVVVDKESTMSAEEDYMADAKTIVNVQTMFRLFPSLSITTELTHPSNMRFMQFRAKDSY rSLACK
901 NLVVVDKESTMSAEEDYMADAKTIVNVQTMFRLFPSLSITTELTHPSNMRFMQFRAKDSY KIAA1422

918 SLALSKLEKRENGSNLAFMFRLPFAAGRVSISM LDTLLYQS FVKDYMITITRLL LGL hSlo2
918 SLALSKLEKQERENGSNLAFMFRLPFAAGRVSISM LDTLLYQS FVKDYMITITRLL LGL rSLACK
961 SLALSKLEKRENGSNLAFMFRLPFAAGRVSISM LDTLLYQS FVKDYMITITRLL LGL KIAA1422

978 DTPGSGGYLCAMKITEGDLWIRTYGR L FQKLCSSSAEIPIGIYRTE SHVFS TSEPHDLRA hSlo2
978 DTPGSGGYLCAMKVTEGDLWIRTYGR L FQKLCSSSAEIPIGIYRTE CHVFS -SEPHDLRA rSLACK
1021 DTPGSGGYLCAMKITEGDLWIRTYGR L FQKLCSSSAEIPIGIYRTE SHVFS TSEPHDLRA KIAA1422

FIG. 1 (CONT.)



1038QSQISVNVEDCEDTREVKGPWGSRAGTGGSS-QGRHTGGGDPAEHPLLRRKSLQWARRLS hSlo2
1037QSQISVNVEDCEDTREAKGPWGTRAASGGGSTHGRHGGSSADPVEHPLLRRKSLQWARKLS rSLACK
1081QSQISVNVEDCEDTREVKGPWGSRAGTGGSS-QGRHTGGGDPAEHPLLRRKSLQWARRLS KIAA1422

1097RKAPKQAGRAA-AAEWISQQRLSLYRRSERQELSELVKNRMKHLGLPTTGYEDVANLTAS hSlo2
1097RKSSKQAGKAPMTTDDWITQQRLSLYRRSERQELSELVKNRMKHLGLPTTGYEDVANLTAS rSLACK
1140RKAPKQAGRAA-A KIAA1422

1156DVMNRVNLGYLQDEMNDH-QNTLSYVLINPPPDTRLEPSDIVYLIIRSDPLAHVASSSQSR hSlo2
1157DVMNRVNLGYLQDEMNDHHQNTLSYVLINPPPDTRLEPNDIVYLIIRSDPLAHVTSSSSQSR rSLACK
KIAA1422

1215KSSCASHKLSSCNPETRDETQL hSlo2
1217KSSCSNKLSSCNPETRDETQL rSLACK
KIAA1422

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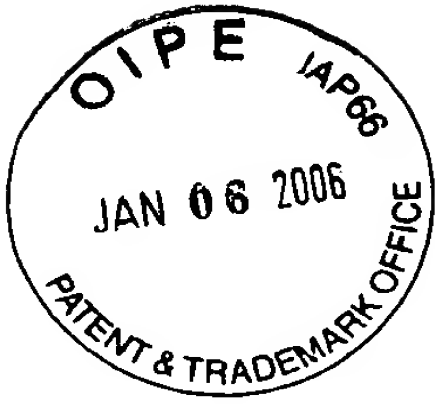
FIG. 1 (CONT.)



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1 MV-----DLESEVPLPRYRFRDLLL---GDQGWQNDDR-----S104
1 MARAKLPRSPSEKAGPGGAPAGAAPEEPH-GLSPLLPARGGSGSDVGQRLPVEDFS S102
33 ---VQVEFYMNENTFKERLKLFFIKNQSSLRIRLFNPSLKLSCLLYIIRVLLLEN S104
60 LDSSLSQVQVEFYVNENTFKERLKLFFIKNQSSLRIRLFNPSLKLTCLLYIVRVLLDD S102
86 PSQGN-----EWSHIFWVNRSLPLWGLQVSVALISLFFETILLGYLS S104
120 PALGIGCWGCPKQNYSFNDSSSEINWAPILMVERKMTLWAIQVIVAIISFLETMLLIYLS S102
127 YKGNIEWEQILRIPIFILEIINAVPFIISIFWPSLRNLFVPVFLNCWLAKHALENMINDLHR S104
180 YKGNIEWEQIFRVSRLVLEMINLTLPFIITIFWPPLRNLFIPVFLNCWLAKHALENMINDFHR S102
187 AIQRTQSAMFNQVLILISTLLCLIFTCCIGIQHLERIGKKLNLFDSL YFCIVTFSTVGF S104
240 AILRTQSAMFNQVLILFCTLLCLVFTGTCCIGIQHLERAGENLSLLTSFYFCIVTFSTVGYG S102
247 DVTPETWSSKLFVVAMICVALVLP IQFEQLAYLWMERQKSGGNYSRHRAQTEKHVVLCV S104
300 DVTPKIWPSQLLVVIMICVALVLP LQFEELVYLWMERQKSGGNYSRHRAQTEKHVVLCV S102
306 SSLKIDLLMDFLNEFYAHPRLQDYVVVILCPTEMDVQVRRVLQIPMWSQRVIYVLQGSALK S104
360 SSLKIDLLMDFLNEFYAHPRLQDYVVVILCPTEMDVQVRRVLQIPLWSQRVIYVLQGSALK S102
367 DQDLLRAKMDDAEACFILSSRCEVDRTSSDHQTIILRAWAVKDFAPNCPLYVQILKPENKF S104
420 DQDLMRAKMDNGEACFILSSRNEVDRTAADHQTIILRAWAVKDFAPNCPLYVQILKPENKF S102
427 HIKFADHVVCHEEFKYAMLALNCICPATSTLITLLVHTSRGQEGQSQPEQWKMYGRC SG S104
460 HVKFADHVVCHEEFKYAMLALNCICPATSTLITLLVHTSRGQEGQSQPEQWKMYGRC SG S102
487 NEVYHIVLEESTFFAEYEGKSFTYASFHAHKKFGVCLIGVRRREDNKNILLNPGPRYIMNS S104
540 NEVYHIRMGDSKFFREYEGKSFTYAAFHAHKKYGVCLIGLKREDNKSILLNPGPRHILAA S102
547 TDICFYINITKEENSAF--KNQDQQRKSNVS-RSFYHGPSRLPVHSIIASMGTVAIDLQD S104
600 SDTCFYINITKEENSAFIFKQEEKRKKRAFSGGGLHEGPRLPVHSIIASM--VAMD LQG S102

FIG. 2



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604 TSCRSA-----SGPTLSLPTEGSKERRPSIAPVLEVADTSSIQTCDLLSDQSEDETP S104
658 TEHRPTQSGGGGSKLALPTENGSGSRRPSIAPVLELADSSALLPCDLLSDQSEDEVTP S102
658 -DEEMSSNLEYAKGYPPYSPYIGSSPTFCHLLHEKVPFCCLRLDKSCQHNYVEDAKAYGF S104
718 SDEGLSVVEYVKGYPNPNPYIVSSPTLCHLLPVKAPFCCLRLDKGCKHNSYEDAKAYGF S102
717 KNKLIIVAAETAGNGLYNFIVPLRAYYRPKKELNPIVLLLDNPPDMHFLDAICWFPMVYY S104
778 KNKLIIVSAETAGNGLYNFIVPLRAYYRSRKELNPIVLLLDNKPDDHFFLEAICCFPMVYY S102
777 MVGSI DNLDLLRCGVTF AANMVVDKESTMSAEEDYMADAKTIVNVQTLFRFSSLSII S104
838 MEGSV DNLDLSLLQCGIIYADNLVVVDKESTMSAEEDYMADAKTIVNVQTMFRFSPSLSIT S102
837 TELTHPANRMFMQFRAKDCYSLALSLEKKERERGSNLA FMFRLPFAAGRVSISM LDTL S104
898 TELTHPSNMRFMQFRAKDSYSLALSLEKKERERENG SNLA FMFRLPFAAGRVSISM LDTL S102
897 LYQSFVKDYMITITRLLGLDTPGSGFLCSMKITADDLWIRTYARLYQKLCSS TGDVPI S104
958 LYQSFVKDYMITITRLLGLDTPD SGYLCAMKITEGDLWIRTYGR LFQKLCSSSAE IPI S102
957 GIYRTESQKLTSE-----SQISISVEEWEDTKDSKEQGHR-----SNHRNSTSSD S104
1018 GIYRTESHVFTSEPHDLRAQSQISVNVEDCEDTREVKGPWGSRAGTGGSSQGRHTGGGD S102
1004 QSDHPLLRKSMQWARRLSRKGPKHSGKTA--EKITQQRLNLYRRSERQELAE LVKNRMK S104
1078 PAEHPLLRKSLQWARRLSRKAPKQAGRAAAAEWISQQRLSLYRRSERQELSELVKNRMK S102
1062 HLGLSTVGY-----DEMDHQSTLSYILINPSPDTRIELNDVVY S104
1138 HLGLPTTG YEDVANLTASDVMMNRVNLGYLQDEMDHQNTLSYVLINPPDTRLEPSDIVY S102
1101 LIRPDPLAYLPNSEPSRRNSICNVT---GQDSREETQL. S104
1198 LIRSDPLAHAVASSQSRKSS-CSHKLSSCNPETRDETQL. S102

FIG. 2 (CONT.)



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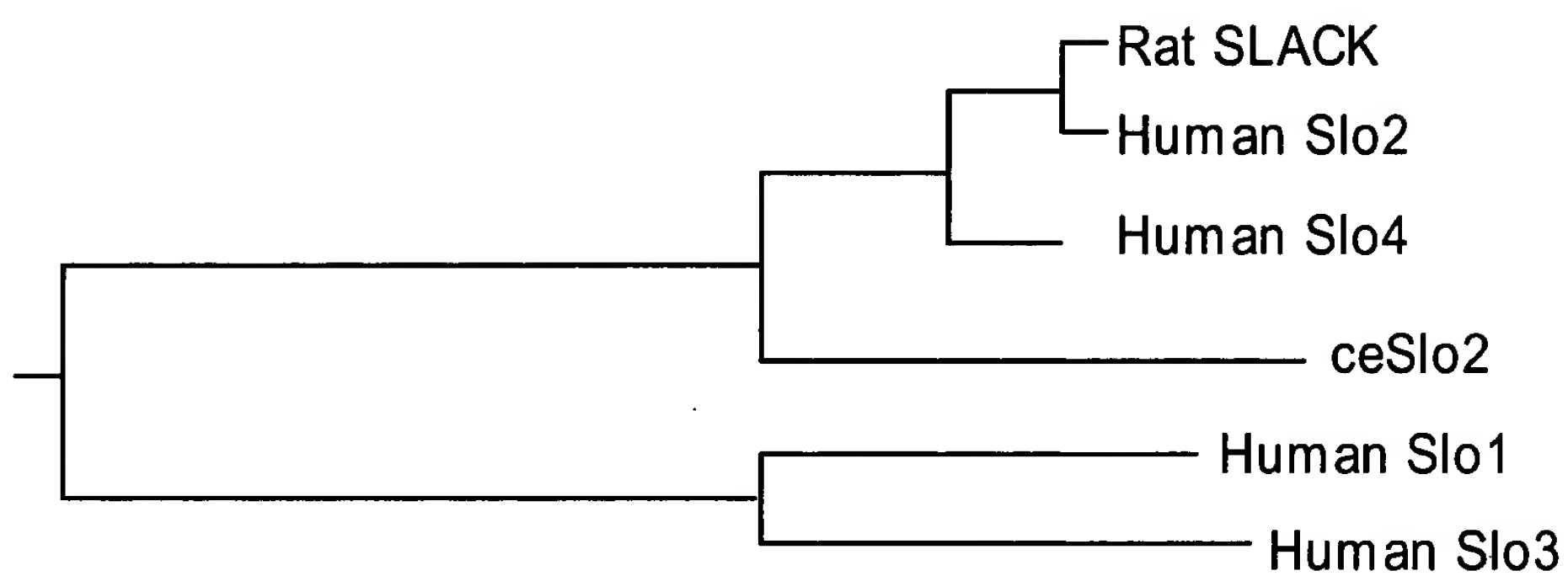


FIG. 3



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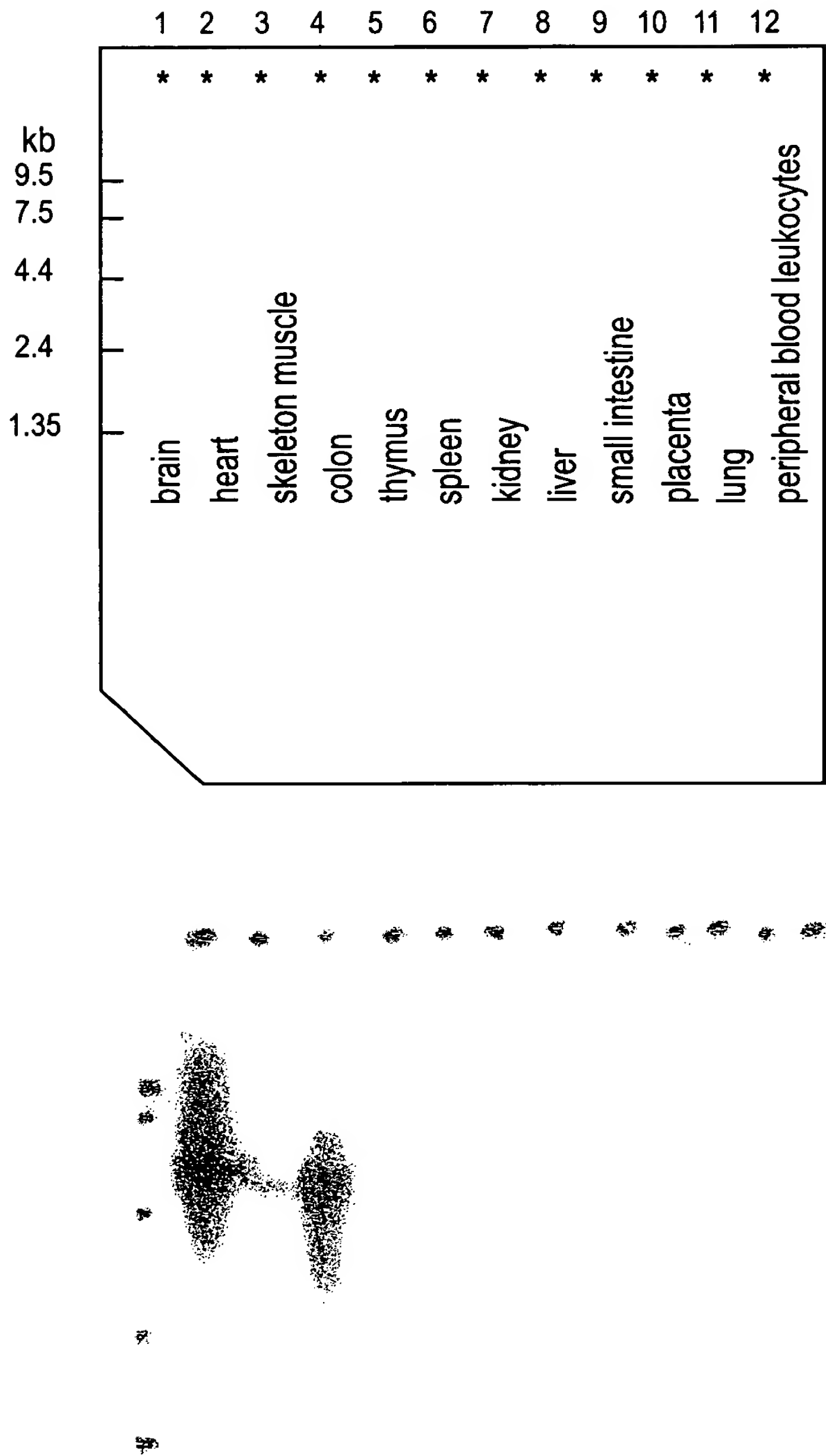


FIG. 4A



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	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
C	heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast total RNA 100 mg	yeast tRNA 100 mg	E. coli rRNA 100 mg	E. coli DNA 100 mg	poly r(A) 100 mg	human Cot-1 DNA 100 mg	human DNA 100 mg	human DNA 500 mg
	1	2	3	4	5	6	7	8

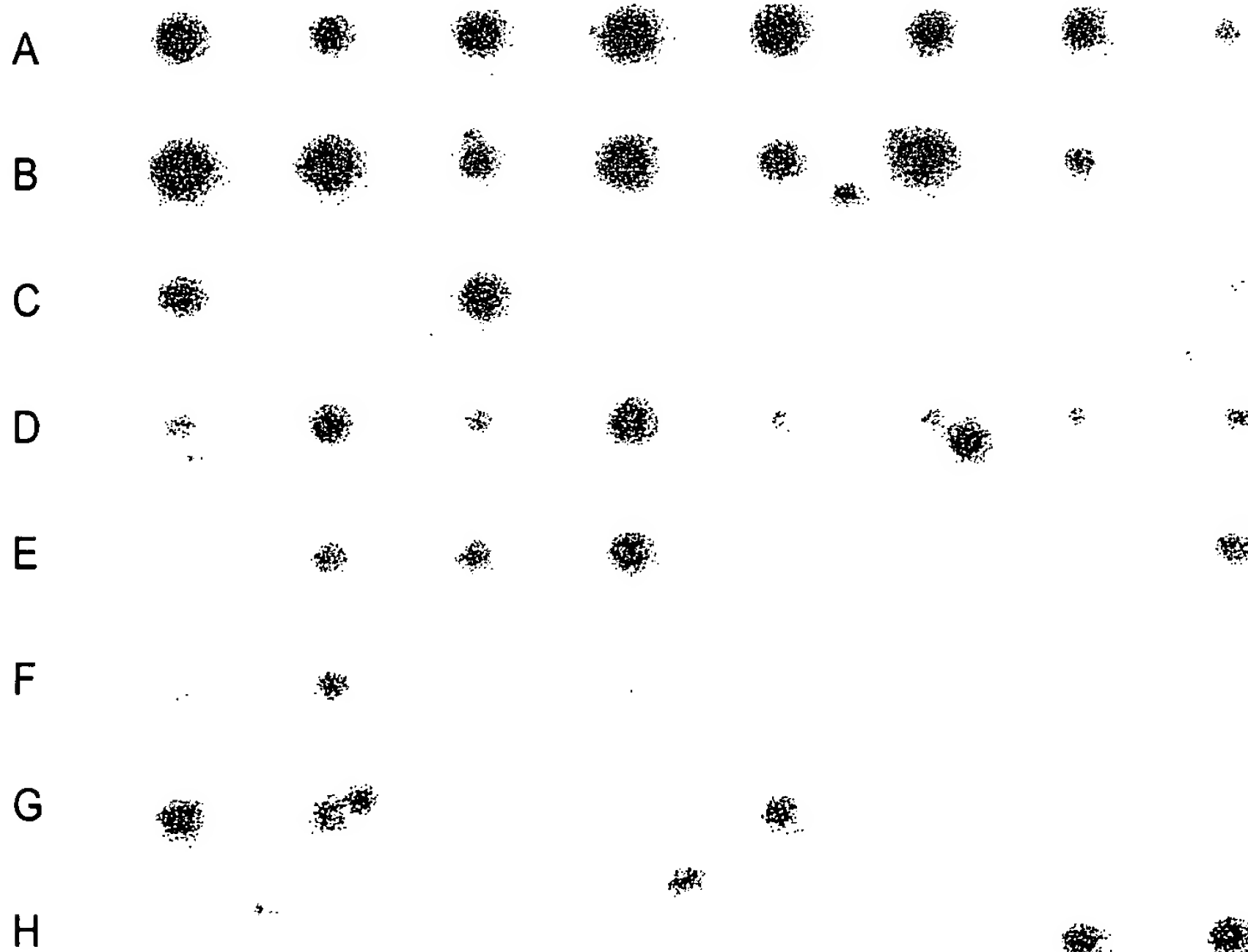


FIG. 4B



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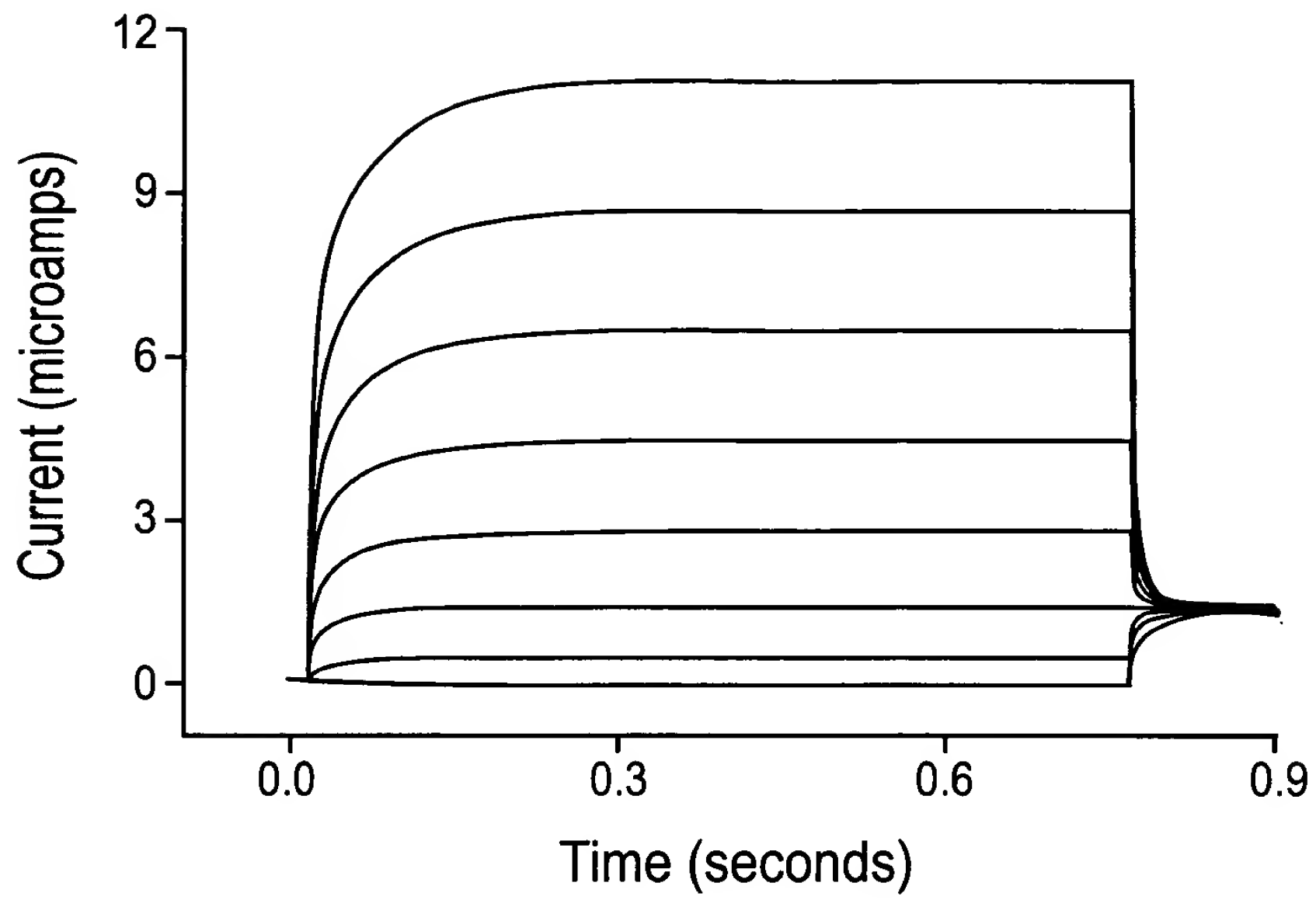


FIG. 5A

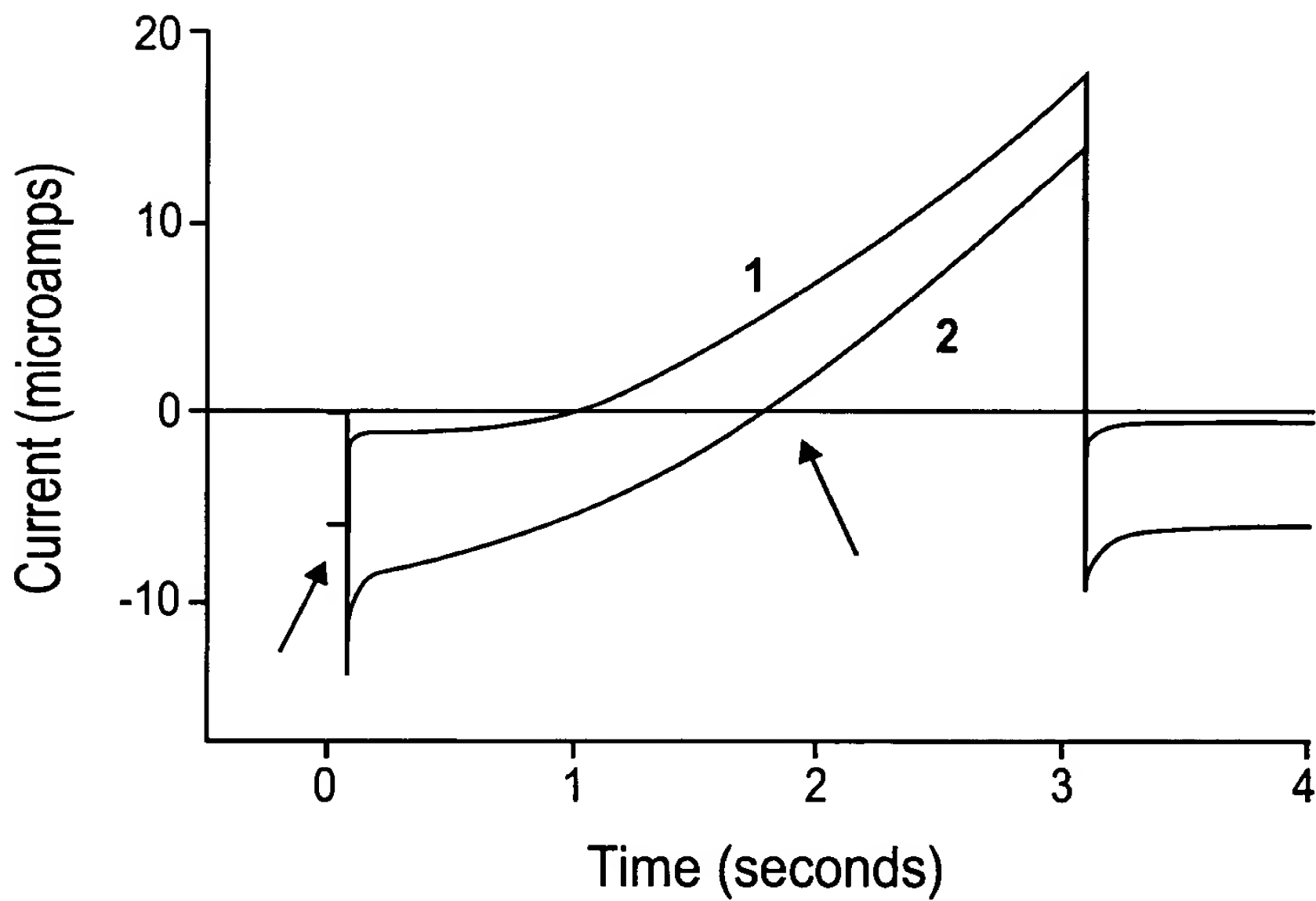


FIG. 5B



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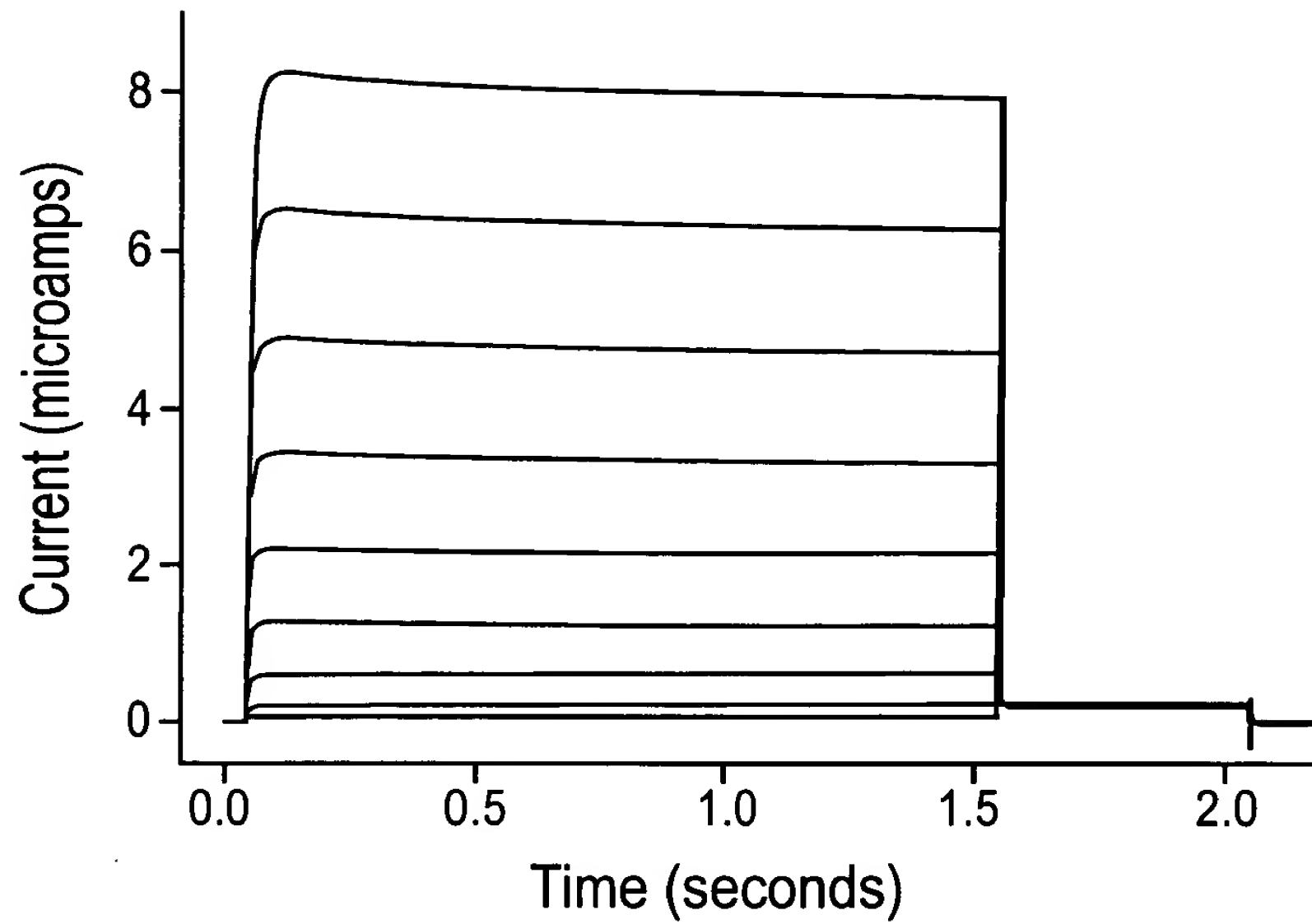


FIG. 6A

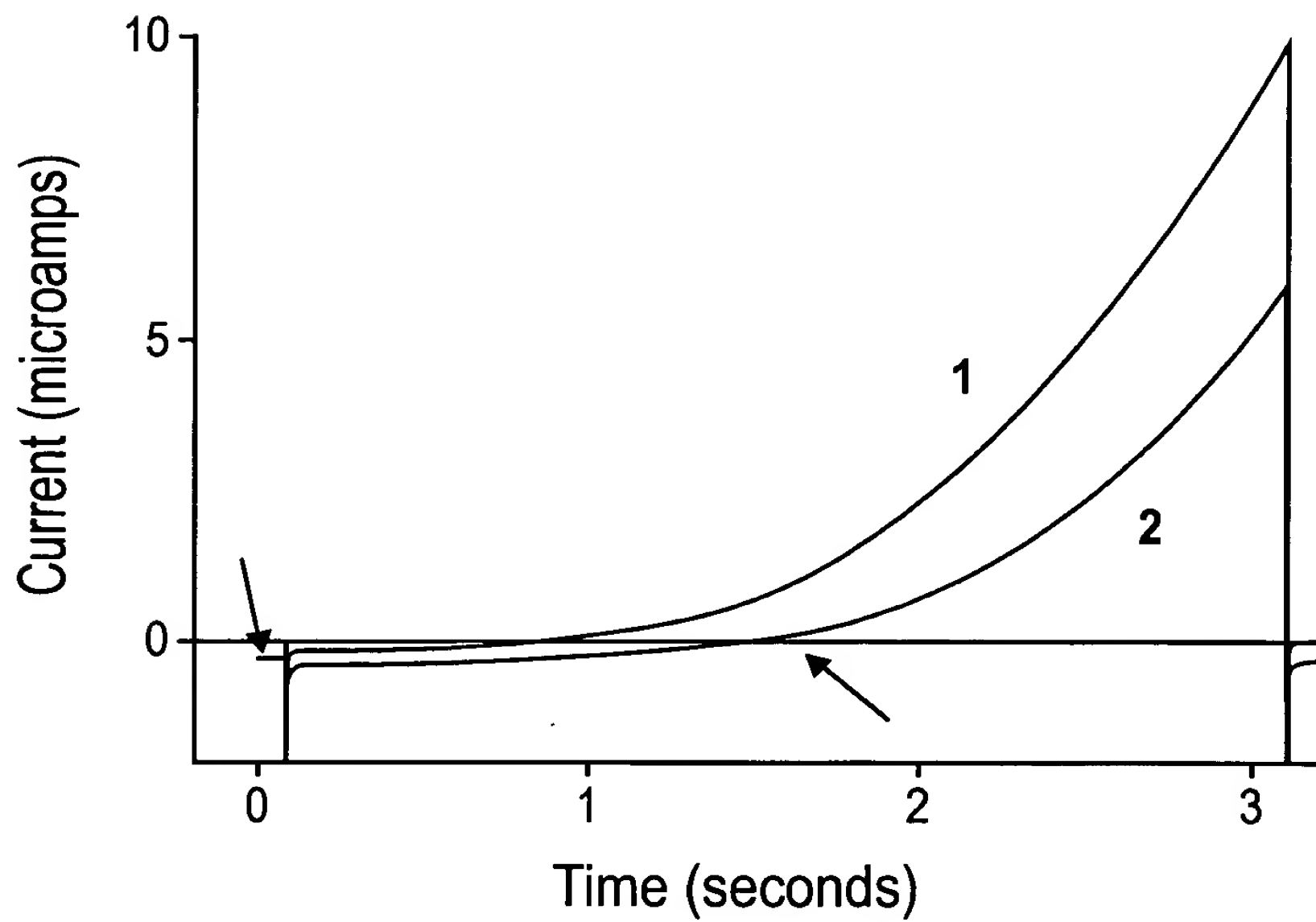


FIG. 6B



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Slo4 Northern Blot

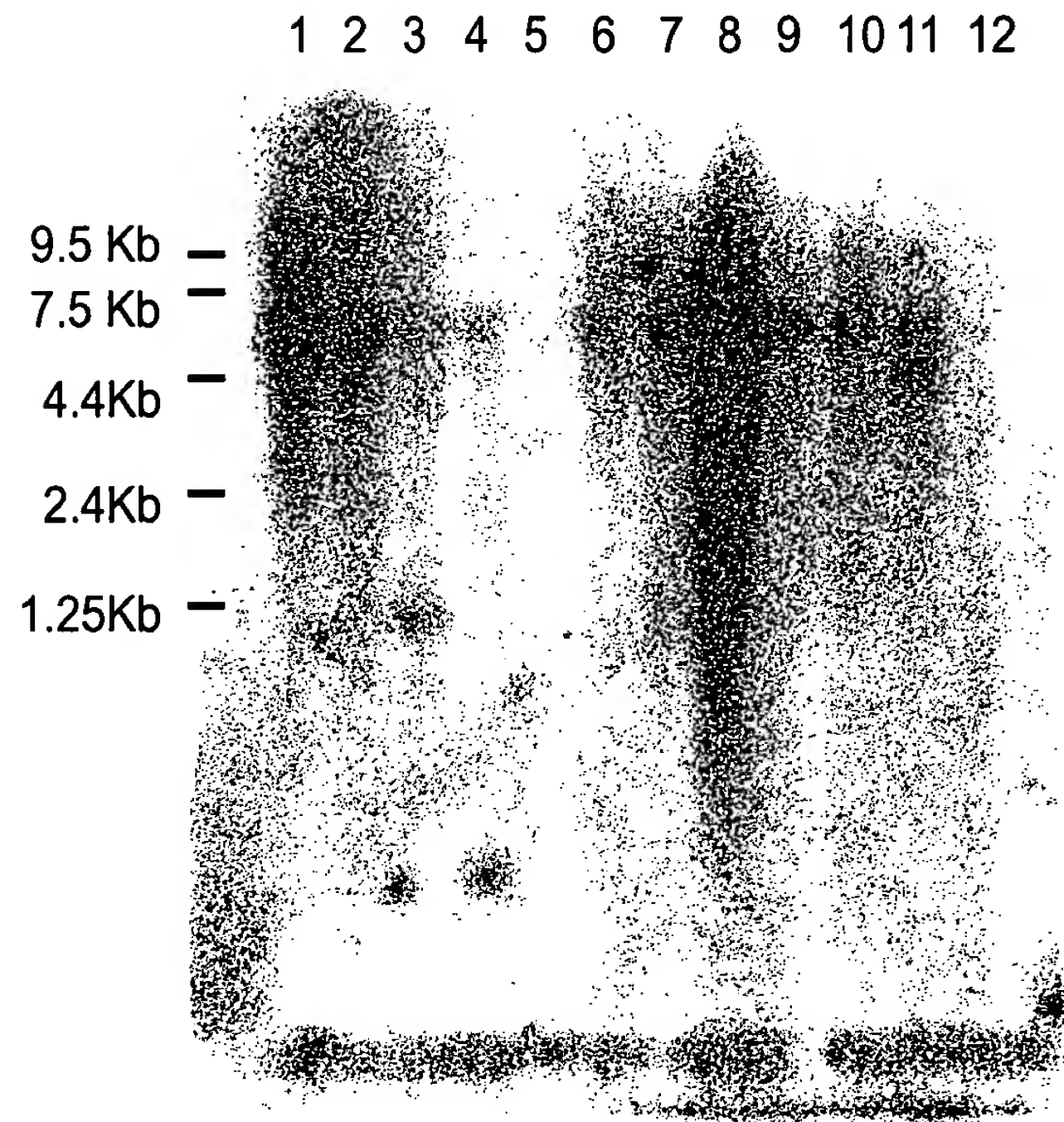


FIG. 7A



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Slo4 mRNA Dot Blot

	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum, left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum, right	nucleus accumbens	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	Hela	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia, K-562	fetal kidney	E. coli rRNA
D	parietal lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	E. coli DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle, left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	poly r(A)
F	temporal lobe	hippo-campus		ventricle, right	ileocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human C ₀ t1 DNA
G	p. g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma, SW480	fetal lung	human DNA 100 mg
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma, A549		human DNA 500 mg

* paraconitral gyrus

FIG. 7B



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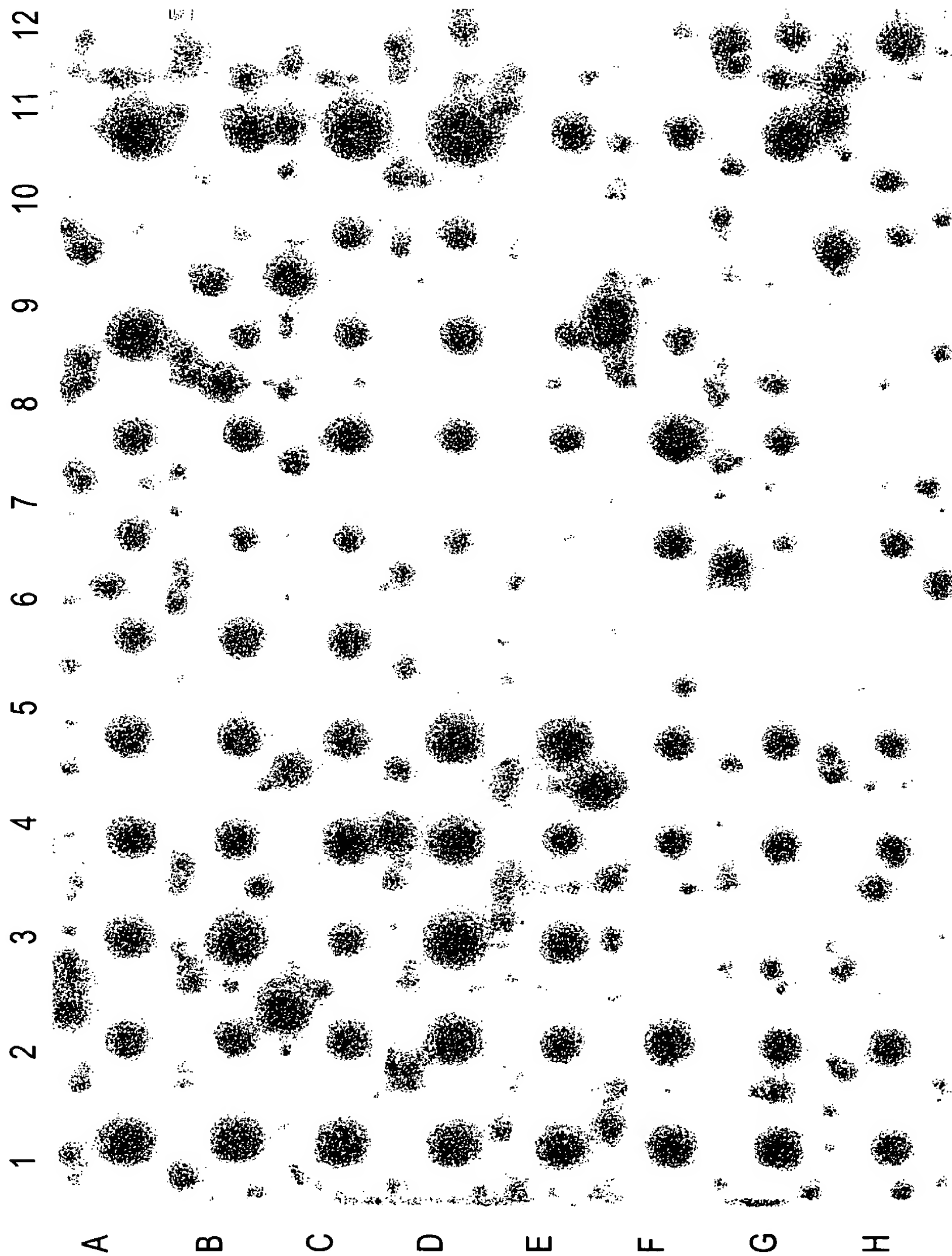


FIG. 7B (CONT.)